

SOFTWARE: pt_sp_genes Version 1.0
SEQ ID NO 1525
LENGTH: 886
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: sig peptide
LOCATION: (70)...(205)
OTHER INFORMATION: this location contains the signal peptide sequence,
OTHER INFORMATION: MGMTMLVTAALLGLMMVVVTGDBDENSPCAHEALLDEDTLFCOG, Run with signalp
FEATURES:
NAME/KEY: misc feature
LOCATION: (304)...(700)
OTHER INFORMATION: similar to gi510339 in the genepept database release 114,
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-491-404-1525

Alignment Scores:
Pred. No.: 0 Length: 886
Score: 1110.00 Matches: 220
Percent Similarity: 96.9% Conservative: 2
Best Local Similarity: 96.1% Mismatches: 1
Query Match: 92.2% Indels: 6
DB: 1 Gaps: 0

US-10-035-958-61-COPY (1-223) x US-09-491-404-1525 (1-886)

QY 1 MetGlyTrrMetArgLeuValThrAlaAlaLeuLeuLeuGlyLeuMetMetValVal 20
Db 70 ATGGTTGGACATGAGGCTGGTCACAGCAGCAGCTGTACTGGGTCTCATGATGGTGGTC 129
QY 21 ThrGlyAspGluAspGluSerProCysAlaHisGluAlaLeuLeuAspGluAspThr 40
Db 130 ACTGGAGACGAGGATGAGAACCGCCGTTGCCCTGAGGCCCTCTTGACGAGCAGCACC 189
QY 41 LeuPheCysGlnGlyLeuGluValPheTyrProGluLeuGlyAsnIleGlyCysGlyVal 60
Db 190 CTCCTTTGCCAGGGCCCTTCAAGTTTCTACCAAGATGGGGAAACATTTGGCTGCAAGGTT 249
QY 61 ValProAspCysAsnSerTyrArgGlnValThrGlnValThrSerTyrMetGluProIleValys 80
Db 250 GTTCTGATTGTAACTACAGACAGAGATCACTTCTGGATGAGGCCGATAGTCAAG 309
QY 81 PheProGlyAlaValAspGlyAlaThrTyrIleLeuValMetValAspProAspAlaPro 100
Db 310 TTCCCGGGGGCGGTGGACGCGCAACCTATATCTGGTGGTGGATCCAGATGCCCT 369
QY 101 SerArgAlaGluProArgGlnArgPheTrrPheHisArgTyrGln-PhePheValTyrLeuGlnGlu-G 120
Db 370 AGCAGAGCAGAACCCACAGACAGAGATCTGGAGACATTTGGCTGGTAAACAGATATCAAGGC 429
QY 121 AlaAspLeuLysGlyLysIleGlnGlyGlnGluLeuSerAla-TyrGlnAlaProSe 140
Db 430 GCCGACCTTGAAGAGGAGGAGATTCAGGGCCAGGAGTTATCAGCCCTACAGGCTCCCTC 489
QY 140 r-ProProAlaHisSerGly-PheHisArgTyrGln-PhePheValTyrLeuGlnGlu-G 159
Db 490 CCCCACCGGCACACAGTGGCTTCCATCGCTACCAAGTCTTTGTCTATCTTCAGAAAGG 549
QY 159 IlyIysValIleSerLeuLeuProLysGluAsnLysThrArgGlySerTrrPlysMetAspA 179
Db 550 GAAAGATCATCTCTCTCTTCCCAAGAAACAAACAACTCCGAGGCTCTTGGAAATGGACA 609
QY 179 rgPheLeuAsnArgPheHisLeuGlyGluProGluAlaSerThrGlnPheMetThrGlnA 199
Db 610 GATTCTGAACCGTTTCCACTGGCGGAACCTTGAAGCAGCAGCAGGCTTCATGACCCAGA 669
QY 199 snTyrGlnAspSerProThrLeuGlnAlaProArgGlyArgAlaSerGluProLysHis- 218
Db 670 ACTACAGGACTCACCACCTCCAGCTCCCAAGAAAGGCCGCGAGCCCAAGCAGACA 729
QY 219 LysThrArgGlnArg 223

OM protein - nucleic search, using frame_plus_p2n model
Run on: June 23, 2006, 15:58:13 ; Search time 0.001 Seconds
(without alignments)
395.156 Million cell updates/sec

Title: US-10-035-958-61-COPY
Perfect score: 1204
Sequence: 1 MGMTMLVTAALLGLMMVV.....PTLQAPRGASEPKHKTRQR 223

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 886 residues
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=soft -Q=new.pep -DB=US09491404.seq -SUFFIX=pto
-OUT=kokler.res -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1
-END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : US09491404.seq.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

		SUMMARIES			
Result	Query				
No.	Score	Match	Length	ID	Description
1	1110	92.2	886	1	US-09-491-404-1525 Sequence 1525, Ap
2	55	4.6	886	1	US-09-491-404-1525 Sequence 1525, Ap

ALIGNMENTS

RESULT 1
US-09-491-404-1525
Sequence 1525, Application US/09491404
GENERAL INFORMATION:
APPLICANT: Tang, Yuanhua T.
APPLICANT: Tillinghaast, John
APPLICANT: Sinku, Ankura
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 785
CURRENT APPLICATION NUMBER: US/09/491.404
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 3796

kokler.res

Fri Jun 23 15:58:31 2006

DB 730 AAAACAGCGGAG 744

RESULT 2

US-09-491-404-1525/c

; Sequence 1525, Application US/09491404

; GENERAL INFORMATION:

; APPLICANT: Tang, Yuanhua T.

; APPLICANT: Tillinghast, John

; APPLICANT: Sinku, Ankura

; APPLICANT: Liu, Chenghua

; APPLICANT: Dmanac, Radoje T.

; TITLE OF INVENTION: Novel Contigs Obtained

; TITLE OF INVENTION: From Various Libraries

; FILE REFERENCE: 785

; CURRENT APPLICATION NUMBER: US/09/491.404

; CURRENT FILING DATE: 2000-01-27

; NUMBER OF SEQ ID NOS: 3796

; SOFTWARE: DT_SP_genes Version 1.0

; SEQ ID NO 1525

; LENGTH: 886

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: (70)...(205)

; OTHER INFORMATION: this location contains the signal peptide sequence, with SignalP

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (304)...(700)

; OTHER INFORMATION: similar to gi510339 in the genepept database release 114,

; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters

; US-09-491-404-1525

Alignment Scores:

Pred. No.: 0 Length: 886

Score: 55.00 Matches: 28

Percent Similarity: 38.4% Conservative: 15

Best Local Similarity: 25.0% Mismatches: 35

Query Match: 4.6% Indels: 35

DB: 1 Gaps: 5

US-10-035-958-61-COPY (1-223) x US-09-491-404-1525 (1-886)

QY 64 CysAsnAsnTyArgGlnLysIleThrSerTrpMetGluProIleValLysPheProGly 83

DB 647 TGTTCAGTTCGCCAGGTGGAACG-----GTTCAAAATCTGTCCATTTCCAGA 594

QY 84 AlaValAspGlyAlaThrTyrIleLeuValMetValAspProAspAlaProSerArgAla 103

DB 593 GCC-----TCGAGTTTGTTCCTTGGGAGGAGAGATGACTTTCCCTCCT 543

QY 104 GluProArgGlnArgPheTrpArgHisTrpLeuValThrAspIleLysGlyAlaAspLeu 123

DB 542 GAGATAGACAGAACTGTGATGCGATG-----AAGGCCACTGTGTGC 498

QY 124 LysLysGlyLysIleGlnGlu----- 132

DB 497 CGTGGGGAGGAGCGCTGTAGGCTGATACTCTGGCCCTGAATCTCCCTTCCTTC 438

QY 133 -----LeuSerAlaTyrGlnAlaProSerProAlaHisSerGlyPhe 147

DB 437 AGGTGCGGCGCCTTGATATCTGT-TACAGCCCAATGTCTCCAGAAATCTCTGTCTGGGTTTC 379

QY 148 -----HisArgTyrGln 151

DB 378 TGCTCTGTAGGGCATCTGGATCCACCATCACCAG 343

Search completed: June 23, 2006, 15:58:13

Job time : 0.001 secs